SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: SHIBAYAMA, SHIRO HIRANO, ATSUSHI OHNO, HIROYUKI
 - (ii) TITLE OF INVENTION: A NOVEL POLYPEPTIDE AND DNAS ENCODING IT
 - (iii) NUMBER OF SEQUENCES: 6
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 - (B) STREET: 2100 Pennsylvania Avenue, N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20037-3202
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 123155/1994
 - (B) FILING DATE: 12-MAY-1994
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)293-7060
 - (B) TELEFAX: (202)293-7860
 - (C) TELEX: 6491103
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Thr Ala Gly Ala Met Gln Leu Cys Trp Val Ile Leu Gly Phe -24 -20 -15 -10

Leu	Phe	Arg -5	GLy	His	Asn	Ser	GIn 1	Pro	Thr	Met	Thr 5	Gln	Thr	Ser
Ser 10	Gln	Gly	Gly	Leu	Gly 15	Gly	Leu	Ser	Leu	Thr 20	Thr	Glu	Pro	Val
Ser	Asn	Pro	Gly	Tyr 30	Ile	Pro	Ser	Ser	Glu 35	Ala	Asn	Arg	Pro	Ser 40
Leu	Ser	Ser	Thr 45	Gly	Thr	Pro	Gly	Ala 50	Gly	Val	Pro	Ser	Ser 55	Gly
Asp	Gly	Gly 60	Thr	Ser	Arg	Asp	Thr 65	Phe	Gln	Thr	Val	Pro 70	Pro	Asn
Thr	Thr 75	Met	Ser	Leu	Ser	Met 80	Arg	Glu	Asp	Ala	Thr 85	Ile	Leu	Pro
Pro 90	Thr	Ser	Glu	Thr	Val 95	Leu	Thr	Val	Ala	Ala 100	Phe	Gly	Val	Ile
Phe	Ile	Val	Ile	Leu 110	Val	Val	Val	Val	Ile 115	Ile	Leu	Val	Gly	Val 120
Ser	Leu	Arg	Phe 125	Lys	Cys	Arg	Lys	Ser 130	Lys	Glu	Ser	Glu	Asp 135	Pro
Lys	Pro	Gly 140	Ser	Ser	Gly	Leu	Ser 145	Glu	Ser	Cys	Ser	Thr 150	Ala	Asn
Glu	Lys 155	Asp	Ser	Ile	Thr	Leu 160	Ile	Ser	Met	Lys	Asn 165	Ile	Asn	Met
Asn 170	Gly	Lys	Gln	Ser	Leu 175	Ser	Ala	Glu	Lys	Val 180	Leu			
INFO	RMA	rion	FOR	SEQ	I DI	10:2:								
(i) SEQUENCE CHARACTERISTICS:														
	Ser 10 Ser Leu Asp Thr Pro 90 Phe Ser Lys Glu Asn 170 INFO	Ser Asn Leu Ser Asp Gly Thr Thr 75 Pro Thr 90 Phe Ile Ser Leu Lys Pro Glu Lys 155 Asn Gly INFORMAY (i) SEG	Ser Asn Pro Leu Ser Ser Asp Gly Gly 60 Thr Thr Met 75 Pro Thr Ser 90 Phe Ile Val Ser Leu Arg Lys Pro Gly 140 Glu Lys Asp 155 Asn Gly Lys 170 INFORMATION (i) SEQUENC	Ser Asn Pro Gly Leu Ser Ser Thr 45 Asp Gly Gly Thr 60 Thr Thr Met Ser 75 Pro Thr Ser Glu 90 Phe Ile Val Ile Ser Leu Arg Phe 125 Lys Pro Gly Ser 140 Glu Lys Asp Ser 155 Asn Gly Lys Gln 170 INFORMATION FOR (i) SEQUENCE CF	Ser Gln Gly Gly Leu Ser Asn Pro Gly Tyr 30 Leu Ser Ser Thr Gly 45 Asp Gly Gly Thr Thr Met Ser Leu 75 Thr Ser Glu Thr Pro Thr Ser Glu Thr 90 Thr Ser Glu Thr Phe 11e Val 11e Leu 110 Ser Leu Arg Phe Lys Lys Pro Gly Ser Ser Glu Lys Asp Ser 11e Asn Gly Lys Gln Ser 110 Sequence Characteric (i) Sequence Characteric Ser Ser Characteric Ser Ser Characteric Characteric Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	Ser Gln Gly Gly Leu Gly 15	Ser Gln Gly Gly Leu Gly Gly Ser Asn Pro Gly Tyr Ile Pro 30 Thr Pro Gly Thr Pro Asp Gly Gly Thr Ser Arg Asp 60 Thr Ser Leu Ser Met 75 75 For Glu Thr Val Leu 90 Thr Ser Glu Thr Val 110 Val Thr Leu 125 Asp Ser Ser Gly Leu 160 Asn Gly Lys Gln Ser Leu Ser 170 Thr Ser Ser Thr Ser 180 Thr Ser Thr Ser 180 Thr Ser Thr Ser 180 Thr Thr Thr 180 Thr Thr Thr 180 Thr Thr Thr 180 Thr Thr Thr 180 Thr 180 Thr Thr 180 Thr	Ser Gln Gly Gly Leu Gly Gly Leu Ser Asn Pro Gly Tyr Ile Pro Ser Leu Ser Ser Thr Gly Thr Pro Gly Asp Gly Gly Thr Ser Arg Asp Thr 65 Thr Thr Met Ser Leu Ser Met Arg Roy Thr Ser Glu Thr Val Leu Thr 90 Thr Ser Glu Thr Val Leu Thr 90 Thr Ser Glu Thr Val Val Val Ser Leu Arg Phe Lys Cys Arg Lys Lys Pro Gly Ser Ser Gly Leu Ser 140 Thr Ser Gly Thr Leu Ile 155 Asp Ser Ile Thr Leu Ile 170 Thr Ser Gln Ser Leu Ser Ala 170 Thr Ser Ser Characteristics:	Ser Gln Gly Gly Leu Gly Gly Leu Ser Asn Pro Gly Tyr Ile Pro Ser Ser Asp Gly Gly Thr Pro Gly Ala So Ser Gly Gly Thr Pro Gly Ala So Asp Gly Gly Thr Pro Gly Ala So Thr Gly Thr Asp Gly Gly Thr Ser Asp Thr Phe GS Thr Thr Met Ser Leu Ser Met Arg Glu Ro Thr Ser Glu Thr Val Leu Thr Val 95 Pro Thr Ser Glu Thr Val Leu Thr Val Ser Leu Arg Phe Lys Cys Arg Lys Ser 125 Lys Pro Gly Ser Ser Gly Leu Ser Glu Glu Lys Asp Ser Ile Thr Leu Ile Ser Asn Gly Lys Gln Ser Leu Ser Ala Glu INFORMATION FOR SEQ ID NO:2:	Ser Gln Gly Gly Leu Gly Gly Leu Ser Leu Ser Asn Pro Gly Tyr Ile Pro Ser Ser Glu 35 Leu Ser Ser Thr Gly Thr Pro Gly Ala Gly Asp Gly Gly Thr Ser Asp Thr Phe Gln 65 Asp Gly Gly Thr Ser Arg Asp Thr Phe Gln 65 Thr Thr Met Ser Leu Ser Met Arg Glu Asp Asp Arg Glu Asp Asp Thr Ser Glu Thr Val Leu Thr Val Ala Ala 95 Pro Thr Ser Glu Thr Val Val Val Val Ile Ili Ser Leu Arg Phe Lys Cys Arg Lys Ser Lys Ili Ser Leu Arg Phe Lys Cys Arg Lys Ser Lys Ili Glu Lys Asp Ser Ile Thr Leu Ile Ser Met Ili Asn Gly Lys Gln Ser Leu Ser Ala Glu Lys Information For Seq Id No:2: (i) SeQUENCE CHARACTERISTICS:	Ser Asn Pro Gly Thr Ser Leu Ser Met Arg Glu Asp Ala 755 Thr Thr Met Ser Leu Ser Met Arg Glu Asp Ala 100 Phe Ile Val Ile Leu Val Val Val Val Ile Val Ile Ser Leu Arg Phe 125 Ser Leu Arg Pro Gly Ser Ser Glu Thr Val Ala Ala 100 Phe Lue Ser Ser Glu Thr Val Val Val Val Ile Ile Ile Val Ile Leu Ser Met Arg Glu Asp Ala 100 Phe Jue Val Ile Leu Val Val Val Val Val Ile Ile Ile Ile Ile Ile Ile Ile Ile Il	Ser Gln Gly Gly Leu Gly Gly Leu Ser Leu Thr Thr 20	Ser Gln Gly Gly Leu Gly Gly Leu Ser Leu Thr Thr Glu Ser Asn Pro Gly Tyr Jle Pro Ser Ser Glu Ala Asn Arg Asp Gly Gly Thr Ser Arg Asp Thr Pro Gly Ala Gly Val Pro Ser Thr Thr Met Ser Leu Ser Met Arg Glu Asp Ala Thr Jle 75 Pro Thr Ser Glu Thr Val Val Val Val Ala Ala Phe Gly 90 Phe Ile Val Ile Leu Yal Val Val Val Ile Ile Leu Val Ser Leu Arg Phe Lys Cys Arg Lys Ser Lys Glu Ser Glu Lys Pro Gly Ser Ser Ile Thr Leu Ile Ser Met Lys Asp 115 Asn Gly Lys Gln Ser Leu Ser Ala Glu Lys Val Leu 1175 INFORMATION FOR SEQ ID NO:2:	Ser Asn Pro Gly Thr Ser Leu Ser Met 80 Thr Val Ala Ala Phe Gly Val Gly Val Gly Val Gly Val Gly Val Gly Val Pro Ser Ser Asp Glu Thr Val Ala Ala Ala Phe Gly Val Pro Pro Thr Ser Glu Thr Val Val Val Val Gly Val Gly Val Gly Val Gly Val Rro Ser Ser Ser Thr Ala Ala Ser Ser Ser Ser Ser Asp Gly Gly Thr Ser Arg Asp Thr Phe Glu Thr Val Pro Pro Res Ser Note of Ser

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGGCACCG	CAGGAGCCAT	GCAGCTGTGC	TGGGTGATCC	TGGGCTTCCT	CCTGTTCCGA	60
GGCCACAACT	CCCAGCCCAC	AATGACCCAG	ACCTCTAGCT	CTCAGGGAGG	CCTTGGCGGT	120
CTAAGTCTGA	CCACAGAGCC	AGTTTCTTCC	AACCCAGGAT	ACATCCCTTC	CTCAGAGGCT	180
AACAGGCCAA	GCCATCTGTC	CAGCACTGGT	ACCCCAGGCG	CAGGTGTCCC	CAGCAGTGGA	240

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AGAGACGGAG	GCACAAGCAG	AGACACATTT	CAAACTGTTC	CCCCCAATTC	AACCACCATG	300
AGCCTGAGCA	TGAGGGAAGA	TGCGACCATC	CTGCCCAGCC	CCACGTCAGA	GACTGTGCTC	360
ACTGTGGCTG	CATTTGGTGT	TATCAGCTTC	ATTGTCATCC	TGGTGGTTGT	GGTGATCATC	420
CTAGTTGGTG	TGGTCAGCCT	GAGGTTCAAG	TGTCGGAAGA	GCAAGGAGTC	TGAAGATCCC	480
CAGAAACCTG	GGAGTTCAGG	GCTGTCTGAA	AGCTGCTCCA	CAGCCAATGG	AGAGAAAGAC	540
AGCATCACCC	TTATCTCCAT	GAAGAACATC	AACATGAATA	ATGGCAAACA	AAGTCTCTCA	600
GCAGAGAAGG	TTCTTTAA					618

(2) INFORMATION FOR SEO ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 983 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCTGCCCGC CACATACCCA GCTGACATGG GCACCGCAGG AGCCATGCAG CTGTGCTGGG 60 TGATCCTGGG CTTCCTCCTG TTCCGAGGCC ACAACTCCCA GCCCACAATG ACCCAGACCT 120 CTAGCTCTCA GGGAGGCCTT GGCGGTCTAA GTCTGACCAC AGAGCCAGTT TCTTCCAACC 180 CAGGATACAT CCCTTCCTCA GAGGCTAACA GGCCAAGCCA TCTGTCCAGC ACTGGTACCC 240 CAGGCGCAGG TGTCCCCAGC AGTGGAAGAG ACGGAGGCAC AAGCAGAGAC ACATTTCAAA 300 CTGTTCCCCC CAATTCAACC ACCATGAGCC TGAGCATGAG GGAAGATGCG ACCATCCTGC 360 CCAGCCCCAC GTCAGAGACT GTGCTCACTG TGGCTGCATT TGGTGTTATC AGCTTCATTG 420 TCATCCTGGT GGTTGTGGTG ATCATCCTAG TTGGTGTGGT CAGCCTGAGG TTCAAGTGTC 480 GGAAGAGCAA GGAGTCTGAA GATCCCCAGA AACCTGGGAG TTCAGGGCTG TCTGAAAGCT 540 GCTCCACAGC CAATGGAGAG AAAGACAGCA TCACCCTTAT CTCCATGAAG AACATCAACA 600 TGAATAATGG CAAACAAAGT CTCTCAGCAG AGAAGGTTCT TTAAAAGCAA CTTTGGGTCC 660 CCATGAGTCC AAGGATGATG CAGCTGCCCT GTGACTACAA GGAGGAAGAG ATGGAATTAG 720 TAGAGGCAAT GAACCACATG TAAATTATTT TATTGTTTCA TGTCTGCTTC TAGATCTAAA 780 GGACACTAGC ATTGCCCCAG ATCTGGGAGC AAGCTACCAA CAGGGGAGAC TCTTTCCTGT 840 ATGGACAGCT GCTGTGGAAA TACTGCCTGC TTCTCCCACC TCCTCAGAGC CACAGGAAAG 900

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AGGAGGTGAC AGAGAGAGA CAAGGAAAGT GATGAGGTGG ATTGATACTT TCTACTTTGC	960
ATTAAAATTA TTTTCTAGCC TGC	983
(2) INFORMATION FOR SEQ ID NO:4:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 983 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA to mRNA	
(vi) ORIGINAL SOURCE:(A) ORGANISM: Homo sapiens(H) CELL LINE: endothelial cell line of umbilical cord vein	L
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 27644 (C) IDENTIFICATION METHOD: by similarity to some other patt	.ern
(ix) FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 2798 (C) IDENTIFICATION METHOD: by similarity with known sequence to an established consensus	e or
(ix) FEATURE:	
(A) NAME/KEY: misc_feature (B) LOCATION: 381464 (C) IDENTIFICATION METHOD: by similarity with known sequenc	e or
(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 99641 (C) IDENTIFICATION METHOD: by similarity with known sequenc to an established consensus	e or
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 312320 (C) IDENTIFICATION METHOD: by similarity with known sequence to an established consensus</pre>	e or
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:::	
GCCTGCCCGC CACATACCCA GCTGAC ATG GGC ACC GCA GGA GCC ATG CAG CTG Met Gly Thr Ala Gly Ala Met Gln Leu -24 -20	53
TGC TGG GTG ATC CTG GGC TTC CTC CTG TTC CGA GGC CAC AAC TCC CAG Cys Trp Val Ile Leu Gly Phe Leu Leu Phe Arg Gly His Asn Ser Gln -15 -10 -5 1	101
CCC ACA ATG ACC CAG ACC TCT AGC TCT CAG GGA GGC CTT GGC GGT CTA	149

Pro	Thr	Met	Thr 5	Gln	Thr	Ser	Ser	Ser 10	Gln	Gly	Gly	Leu	Gly 15	Gly	Leu	
AGT Ser	CTG Leu	ACC Thr 20	ACA Thr	GAG Glu	CCA Pro	GTT Val	TCT Ser 25	TCC Ser	AAC Asn	CCA Pro	GGA Gly	TAC Tyr 30	ATC Ile	CCT Pro	TCC Ser	197
TCA Ser	GAG Glu 35	GCT Ala	AAC Asn	AGG Arg	CCA Pro	AGC Ser 40	CAT H i s	CTG Leu	TCC Ser	AGC Ser	ACT Thr 45	GGT Gly	ACC Thr	CCA Pro	GGC Gly	245
GCA Ala 50	GGT Gly	GTC Val	CCC Pro	AGC Ser	AGT Ser 55	GGA Gly	AGA Arg	GAC Asp	GGA Gly	GGC Gly 60	ACA Thr	AGC Ser	AGA Arg	GAC Asp	ACA Thr 65	293
TTT Phe	CAA Gln	ACT Thr	GTT Val	CCC Pro 70	CCC Pro	AAT Asn	TCA Ser	ACC Thr	ACC Thr 75	ATG Met	AGC Ser	CTG Leu	AGC Ser	ATG Met 80	AGG Arg	341
GAA Glu	GAT Asp	GCG Ala	ACC Thr 85	ATC Ile	CTG Leu	CCC Pro	AGC Ser	CCC Pro 90	ACG Thr	TCA Ser	GAG Glu	ACT Thr	GTG Val 95	CTC Leu	ACT Thr	389
GTG Val	GCT Ala	GCA Ala 100	TTT Phe	GGT Gly	GTT Val	ATC Ile	AGC Ser 105	TTC Phe	ATT Ile	GTC Val	ATC Ile	CTG Leu 110	GTG Val	GTT Val	GTG Val	437
GTG Val	ATC Ile 115	ATC Ile	CTA Leu	GTT Val	GGT Gly	GTG Val 120	GTC Val	AGC Ser	CTG Leu	AGG Arg	TTC Phe 125	AAG Lys	TGT Cys	CGG Arg	AAG Lys	485
AGC Ser 130	AAG Lys	GAG Glu	TCT Ser	GAA Glu	GAT Asp 135	CCC Pro	CAG Gln	AAA Lys	CCT Pro	GGG Gly 140	AGT Ser	TCA Ser	GGG G1y	CTG Leu	TCT Ser 145	533
GAA Glu	AGC Ser	TGC Cys	TCC Ser	ACA Thr 150	GCC Ala	AAT Asn	GGA Gly	GAG Glu	AAA Lys 155	GAC Asp	AGC Ser	ATC Ile	ACC Thr	CTT Leu 160	ATC Ile	581
TCC Ser	ATG Met	AAG Lys	AAC Asn 165	ATC Ile	AAC Asn	ATG Met	AAT Asn	AAT Asn 170	GGC Gly	AAA Lys	CAA Gln	AGT Ser	CTC Leu 175	TCA Ser	GCA Ala	629
GAG Glu	AAG Lys	GTT Val 180	CTT Leu	TAA *	AAGO	CAACI	TT C	GGT	CCCP	AT GA	AGTCC	CAAGO	TA E	SATGO	CAGC	684
TGCC	CTGI	GA C	TACA	AAGGA	G GA	AGAG	SATGO	CAA	TAGI	AGA	GGCA	ATG	AAC C	CACAT	GTAAA	744
PATT	TTTT	ATT G	STTTC	CATGI	C TG	CTTC	TAGA	TCI	'AAAC	GAC	ACTA	AGCAT	TG (CCCC#	AGATCT	804
GGG <i>I</i>	AGCAZ	AGC I	ACC	AACAG	G GG	AGAC	CTCTI	TCC	TGTA	TGG	ACAG	CTGC	CTG I	GGAA	ATACT	864
GCCI	GCTI	CT C	CCAC	CCTCC	T CA	GAGC	CACA	GG <i>I</i>	AAGA	GGA	GGTG	SACAC	SAG A	AGAG <i>P</i>	GCAAG	924
GAAA	AGTG#	ATG A	AGGTO	GGATT	'G A'I	ACTI	TCTA	CTI	TGC	ATTA	PAAA	TATT	TTT C	CTAGO	CTGC	983
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(A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (synthetic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: GGAGCTCGTC GACAGATCTG AATTCCATAT GCCCGGGGCG GCCGCACTAG TGGTAC	56
(2) INFORMATION FOR SEQ ID NO:6:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (synthetic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
CACTAGTGCG GCCCCCGG GCATATGGAA TTCAGATCTG TCGACGAGCT CCTGCA	56

(i) SEQUENCE CHARACTERISTICS: